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SEQIDNO1.ST25
SEQUENCE LISTING

<110> AS-Faktor AB

<120> Novel use

<130> 21016008

<150> GB 0322645.3

<151> 2003-09-26

<160> 2

<170> PatentIn version 3.1

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Met Val Leu Glu Ser Thr Met Val Cys Val Asp Asn Ser Glu Tyr
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Ala Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn			
35	40	45	
aac gtg ggc ctt atc aca ctg gct aat gac tgt gaa gtg ctg acc aca			251
Asn Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr			
50	55	60	
ctc acc cca gac act ggc cgt atc ctg tcc aag cta cat act gtc caa			299
Leu Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln			
65	70	75	
ccc aag ggc aag atc acc ttc tgc acg ggc atc cgc gtc gcc cat ctg			347
Pro Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu			
80	85	90	95
gct ctg aag cac cga caa ggc aag aat cac aag atg cgc atc att gcc			395
Ala Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala			
100	105	110	
ttt gtg gga agc cca gtg gag gac aat gag aag gat ctg gtg aaa ctg			443
Phe Val Gly Ser Pro Val Glu Asp Asn Glu Lys Asp Leu Val Lys Leu			
115	120	125	
gct aaa cgc ctc aag aag gag aaa gta aat gtt gac att atc aat ttt			491
Ala Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe			
130	135	140	
ggg gaa gag gag gtg aac aca gaa aag ctg aca gcc ttt gta aac acg			539
Gly Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr			
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ttg aat ggc aaa gat gga acc ggt tct cat ctg gtg aca gtg cct cct			587
Leu Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro			
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ggg ccc agt ttg gct gat gct ctc atc agt tct ccg att ttg gct ggt			635
Gly Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly			
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gaa ggt ggt gcc atg ctg ggt ctt ggt gcc agt gac ttt gaa ttt gga			683
Glu Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly			
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gta gat ccc agt gct gat cct gag ctg gcc ttg gcc ctt cgt gta tct			731
Val Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser			
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Met Glu Glu Gln Arg His Ala Gly Gly Ala Arg Arg Ala Ala Arg			
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gct tct gct gct gag gcc ggg att gct acg act ggg act gaa gac tca			827
Ala Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser			
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gac gat gcc ctg ctg aag atg acc atc agc cag caa gag ttt ggc cgc			875
Asp Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg			
260	265	270	
act ggg ctt cct gac cta agc agt agt act gag gaa gag gag att gct			923
Thr Gly Leu Pro Asp Leu Ser Ser Ser Thr Glu Glu Glu Glu Ile Ala			
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Ser Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala																																																							
305	310	315		aag gag gag gat gat tac gac gtg atg cag gac ccc gag ttc ctt cag	1067	Lys Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln		320	325	330	335	agt gtc cta gag aac ctc cca ggt gtg gat ccc aac aat gaa gcc att	1115	Ser Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile		340	345	350		cga aat gct atg ggc tcc ctg cct ccc agg cca cca agg acg gca aga	1163	Arg Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg		355	360	365		agg aca aga agg agg aag aca aga agt gag act gga ggg aaa ggg	1208	Arg Thr Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly		370	375	380		tagctgagtc tgcttagggg actggaaagc acgaaataata gggtagatg tggtatctg	1268	taaccattac agcctaaata aagcttggca actttaaaa aaaaaaaaaaaa aaaaa	1323	<210> 2		<211> 382		<212> PRT		<213> human									
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10	15																																						
Arg Asn Gly Asp Phe Leu Pro Thr Arg Leu Gln Ala Gln Gln Asp Ala																																							
20	25	30		Val Asn Ile Val Cys His Ser Lys Thr Arg Ser Asn Pro Glu Asn Asn		35	40	45		Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu		50	55	60		Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro		65	70	75	80	Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala		85	90	95		Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe		100	105	110							
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35	40	45		Val Gly Leu Ile Thr Leu Ala Asn Asp Cys Glu Val Leu Thr Thr Leu		50	55	60		Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro		65	70	75	80	Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala		85	90	95		Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe		100	105	110													
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Thr Pro Asp Thr Gly Arg Ile Leu Ser Lys Leu His Thr Val Gln Pro																																							
65	70	75	80	Lys Gly Lys Ile Thr Phe Cys Thr Gly Ile Arg Val Ala His Leu Ala		85	90	95		Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe		100	105	110																									
75	80																																						
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Leu Lys His Arg Gln Gly Lys Asn His Lys Met Arg Ile Ile Ala Phe																																							
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Lys Arg Leu Lys Lys Glu Lys Val Asn Val Asp Ile Ile Asn Phe Gly
130 135 140

Glu Glu Glu Val Asn Thr Glu Lys Leu Thr Ala Phe Val Asn Thr Leu
145 150 155 160

Asn Gly Lys Asp Gly Thr Gly Ser His Leu Val Thr Val Pro Pro Gly
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Pro Ser Leu Ala Asp Ala Leu Ile Ser Ser Pro Ile Leu Ala Gly Glu
180 185 190

Gly Gly Ala Met Leu Gly Leu Gly Ala Ser Asp Phe Glu Phe Gly Val
195 200 205

Asp Pro Ser Ala Asp Pro Glu Leu Ala Leu Ala Leu Arg Val Ser Met
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Glu Glu Gln Arg His Ala Gly Gly Gly Ala Arg Arg Ala Ala Arg Ala
225 230 235 240

Ser Ala Ala Glu Ala Gly Ile Ala Thr Thr Gly Thr Glu Asp Ser Asp
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Asp Ala Leu Leu Lys Met Thr Ile Ser Gln Gln Glu Phe Gly Arg Thr
260 265 270

Gly Leu Pro Asp Leu Ser Ser Thr Glu Glu Glu Glu Ile Ala Tyr
275 280 285

Ala Met Gln Met Ser Leu Gln Gly Ala Glu Phe Gly Gln Ala Glu Ser
290 295 300

Ala Asp Ile Asp Ala Ser Ser Ala Met Asp Thr Ser Glu Pro Ala Lys
305 310 315 320

Glu Glu Asp Asp Tyr Asp Val Met Gln Asp Pro Glu Phe Leu Gln Ser
325 330 335

Val Leu Glu Asn Leu Pro Gly Val Asp Pro Asn Asn Glu Ala Ile Arg
340 345 350

Asn Ala Met Gly Ser Leu Pro Pro Arg Pro Pro Arg Thr Ala Arg Arg
355 360 365

Thr Arg Arg Arg Lys Thr Arg Ser Glu Thr Gly Gly Lys Gly
370 375 380